

**Supplementary Figure 1 (S1)**: The sequencing library with P5 and P7 flow-cell binding sequences. We used two separate sequencing primers for priming Read 1 and Read 2 on the MiSeq for paired-end sequencing (Table 1). The upper strand (us) sequence (5'- to 3'-end) pairs with its lower strand (ls) in the direction from its 3'- to 5'-end. Arrows point sequencing reaction direction.

**Supplementary Figure**: One Codex sequence alignment report. The analysis of sequence alignment of raw sequencing reads (FASTQ) to viral reference genomes was performed. Viruses are reported as "detected" if ≥20% of the genome is observed at ≥ 10x depth. The Y and X axis represent the genome fold coverage (reads/base) and genome position respectively.

**Supplementary Figure 2 (S2)**: Depth of coverage plot generated by One Codex. The performance chart shows the nucleotide coverage read depth (alignment-based coverage using Minimap2) plotted on a log scale in vertical axis (*y*) and the read length (nucleotide position) on a linear scale in horizontal axis (*x*). The genome coverage for the virus was established based on the read length and depth. One Codex alignment confirmed the detection of each virus in a given sample if only the breadth of genome coverage (percent of genome sequenced that is aligned with reference genome) is ≥20% and as well as the depth of sequencing (number of sequencing reads at each reference nucleotide base) at ≥ 10×.